STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/937,519_

Source: _IFW16_

Date Processed by STIC: _9/19/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 4.2.2 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _09/937,519_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s)____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 09/19/2005
PATENT APPLICATION: US/09/937,519   TIME: 10:23:32

Input Set : A:\66741-013; seq. listing
Output Set: N:\CRF4\09192005\I937519.raw

```
 2 <110> APPLICANT: Krupp, Guido
 4 <120> TITLE OF INVENTION: Detection of nucleic acid amplified products
 6 <130> FILE REFERENCE: 66741-013
 8 <140> CURRENT APPLICATION NUMBER: 09/937,519
 9 <141> CURRENT FILING DATE: 2002-03-05
11 <150> PRIOR APPLICATION NUMBER: PCT/EP99/07127
12 <151> PRIOR FILING DATE: 1999-09-27
14 <150> PRIOR APPLICATION NUMBER: DE 199 15 141.5
15 <151> PRIOR FILING DATE: 1999-03-26
17 <160> NUMBER OF SEQ ID NOS: 202
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4
23 <212> TYPE: DNA
24 <213> ORGANISM: artificial sequence
26 <220> FEATURE:
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of the molecule of DNA/RNA combination:
30       artificial DNA sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
34       RNA sequence
36 <400> SEQUENCE: 1
37 gaaa                                                              4
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 7
42 <212> TYPE: DNA
43 <213> ORGANISM: artificial sequence
45 <220> FEATURE:
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
49       RNA sequence
51 <400> SEQUENCE: 2
52 cuganga                                                           7
55 <210> SEQ ID NO: 3
56 <211> LENGTH: 14
57 <212> TYPE: DNA
58 <213> ORGANISM: artificial sequence
60 <220> FEATURE:
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
64       DNA sequence
66 <400> SEQUENCE: 3
```

W--> (handwritten annotations throughout:)
- "pp 1-7"
- "Does Not Comply / Corrected Diskette Needed" (stamp)
- "delete extra <220> (global error)"
- "artificial — insufficient explanation — give source of genetic material (see item 11 on Error Summary Sheet)"
- "This is also a combined DNA/RNA sequence"
- "delete"
- "insufficient"
- "n's need explanation (see p. 7)"
- "insufficient"

```
 67 tccgagccgg wcgr                                                    14
 70 <210> SEQ ID NO: 4
 71 <211> LENGTH: 16
 72 <212> TYPE: DNA
 73 <213> ORGANISM: artificial sequence
 75 <220> FEATURE:
 77 <220> FEATURE:
 78 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
 79       DNA sequence
 81 <400> SEQUENCE: 4
 82 rggctagcha caacga                                                  16
 85 <210> SEQ ID NO: 5
 86 <211> LENGTH: 13
 87 <212> TYPE: DNA
 88 <213> ORGANISM: artificial sequence
 90 <220> FEATURE:
 92 <220> FEATURE:
 93 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
 94       RNA sequence
 96 <400> SEQUENCE: 5
 97 ggaaucgaaa cgc                                                     13
100 <210> SEQ ID NO: 6
101 <211> LENGTH: 32
102 <212> TYPE: DNA
103 <213> ORGANISM: artificial sequence
105 <220> FEATURE:
106 <221> NAME/KEY: modified base
107 <222> LOCATION: (24)..(25)
108 <223> OTHER INFORMATION: modified nucleotide at position 24:
109       Pyridin-4-one (cf. Burgin et al., 1996)
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
113       RNA/DNA sequence
115 <220> FEATURE:
116 <221> NAME/KEY: modified base
117 <222> LOCATION: (27)..(28)
118 <223> OTHER INFORMATION: modified nucleotide at position 27:
119       Pyridin-4-one (cf. Burgin et al., 1996)
121 <400> SEQUENCE: 6
W--> 122 gcgtctagcg gaaacgctac tgangagatt cc                            32
125 <210> SEQ ID NO: 7
126 <211> LENGTH: 22
127 <212> TYPE: DNA
128 <213> ORGANISM: artificial sequence
130 <220> FEATURE:
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
134       RNA sequence
136 <400> SEQUENCE: 7
```

[Handwritten annotations:] Insufficient — also combined DNA/RNA — artificial — Insufficient — Keep this; but explain source of genetic material on another <223>/line — why isn't this "n" too? (since "n" at location 24 is the same modified nucleotide) — This is also a combined DNA/RNA — Insufficient

```
137 gcagcuaugg aaayguuaaa ag                                    22
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 40
142 <212> TYPE: DNA
143 <213> ORGANISM: artificial sequence
145 <220> FEATURE:
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
149       RNA/DNA sequence
151 <220> FEATURE:
152 <221> NAME/KEY: modified base
153 <222> LOCATION: (29)..(30)
154 <223> OTHER INFORMATION: modified nucleotide at position 29:
155       Pyridin-4-one (cf. Burgin et al., 1996)
157 <400> SEQUENCE: 8
158 ttttaacruc tagcggaaac gctactgang acatagctgc                 40
161 <210> SEQ ID NO: 9
162 <211> LENGTH: 54
163 <212> TYPE: DNA
164 <213> ORGANISM: artificial sequence
166 <220> FEATURE:
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of the artificial sequence: primer
171 <400> SEQUENCE: 9
172 aattctaata cgactcacta tagggtgcta tgtcacttcc ccttggttct ctca   54
175 <210> SEQ ID NO: 10
176 <211> LENGTH: 46
177 <212> TYPE: DNA
178 <213> ORGANISM: artificial sequence
180 <220> FEATURE:
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of the artificial sequence: primer
185 <400> SEQUENCE: 10
186 gaatctcatc agtagcgagt gggggggacat caagcagcca tgcaaa          46
189 <210> SEQ ID NO: 11
190 <211> LENGTH: 28
191 <212> TYPE: DNA
192 <213> ORGANISM: artificial sequence
194 <220> FEATURE:
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
198       RNA sequence
200 <400> SEQUENCE: 11
201 tgaaucgaaa cgcgaaagcg ucuagcgu                               28
204 <210> SEQ ID NO: 12
205 <211> LENGTH: 46
206 <212> TYPE: DNA
207 <213> ORGANISM: artificial sequence
209 <220> FEATURE:
```

W--> 158 (handwritten marking)

(handwritten note near lines 148-153) also, give source of Artificial Sequence on another <223> line

(handwritten note near line 153) (30) (29)

(handwritten note near lines 192-198) also, this is a combined DNA/RNA ... artificial insufficient

RAW SEQUENCE LISTING   DATE: 09/19/2005
PATENT APPLICATION: US/09/937,519   TIME: 10:23:32

Input Set : A:\66741-013; seq. listing
Output Set: N:\CRF4\09192005\I937519.raw

211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of the artificial sequence: primer
214 <400> SEQUENCE: 12
215 gaatctcatc agtagcgagt gggggggacat caagcagcca tgcaaa   46
218 <210> SEQ ID NO: 13
219 <211> LENGTH: 15
220 <212> TYPE: DNA
221 <213> ORGANISM: artificial sequence

also Slw is a combined DNA/RNA

223 <220> FEATURE:
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of the artificial sequence (artificial) *insufficient*
227   RNA sequence   *explanation*
229 <400> SEQUENCE: 13
230 tacguagucc gugcu   15
233 <210> SEQ ID NO: 14
234 <211> LENGTH: 13
235 <212> TYPE: DNA
236 <213> ORGANISM: artificial sequence
238 <220> FEATURE:
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of the artificial sequence: primer
243 <400> SEQUENCE: 14
244 gcgtttcgat tcc   13
247 <210> SEQ ID NO: 15
248 <211> LENGTH: 142
249 <212> TYPE: DNA
250 <213> ORGANISM: Human immunodeficiency virus type 1
252 <220> FEATURE: *delete - ho <2217, <2227, or <2237, nor <2207 is not needed*
254 <400> SEQUENCE: 15
255 agtggggggga catcaagcag ctatgcaaac gttaaaagat actatcaatg aggaagctgc 60
256 agaatgggac agggtacatc cagtacatgc agggcctatt ccaccaggcc agatgagaga 120
257 accaaggggga agtgacatag ca   142
260 <210> SEQ ID NO: 16
261 <211> LENGTH: 24
262 <212> TYPE: DNA
263 <213> ORGANISM: artificial sequence
265 <220> FEATURE:

insufficient

267 <220> FEATURE:
268 <223> OTHER INFORMATION: Description of the artificial sequence: (artificial)
269   DNA sequence
271 <400> SEQUENCE: 16
272 agcagctatg gaaaygttaa aaga   24
275 <210> SEQ ID NO: 17
276 <211> LENGTH: 54
277 <212> TYPE: DNA
278 <213> ORGANISM: artificial sequence
280 <220> FEATURE:
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of the artificial sequence: primer

```
285 <400> SEQUENCE: 17
286 aattctaata cgactcacta tagggagtgg ggggacatca agcagctatg gaaa          54
289 <210> SEQ ID NO: 18
290 <211> LENGTH: 42
291 <212> TYPE: DNA
292 <213> ORGANISM: artificial sequence
294 <220> FEATURE:
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of the artificial sequence: artificial
298      RNA sequence
300 <400> SEQUENCE: 18
301 gggagtgggg ggacatcaag cagctatgga aayguuaaaa ga          42
304 <210> SEQ ID NO: 19
305 <211> LENGTH: 24
306 <212> TYPE: DNA
307 <213> ORGANISM: Escherichia coli
309 <220> FEATURE:
311 <400> SEQUENCE: 19
312 taatgtctgg gaaactgcct gatg          24
315 <210> SEQ ID NO: 20
316 <211> LENGTH: 24
317 <212> TYPE: DNA
318 <213> ORGANISM: Escherichia coli
320 <220> FEATURE:
322 <400> SEQUENCE: 20
323 ataactactg gaaacggtag ctaa          24
326 <210> SEQ ID NO: 21
327 <211> LENGTH: 24
328 <212> TYPE: DNA
329 <213> ORGANISM: Escherichia coli
331 <220> FEATURE:
333 <400> SEQUENCE: 21
334 agtcagatgt gaaatccccg ggct          24
337 <210> SEQ ID NO: 22
338 <211> LENGTH: 24
339 <212> TYPE: DNA
340 <213> ORGANISM: Escherichia coli
342 <220> FEATURE:
344 <400> SEQUENCE: 22
345 gtgtagcggt gaaatgcgta gaga          24
348 <210> SEQ ID NO: 23
349 <211> LENGTH: 24
350 <212> TYPE: DNA
351 <213> ORGANISM: Escherichia coli
353 <220> FEATURE:
355 <400> SEQUENCE: 23
356 gctcaggtgc gaaagcgtgg ggag          24
359 <210> SEQ ID NO: 24
360 <211> LENGTH: 24
```

[Handwritten annotations:] also, this is a combined DNA/RNA — insufficient

[Handwritten annotation at line 309:] delete

[Handwritten annotation at bottom:] Please correct the types of errors shown on these pages, in subsequent sequences

<210> 57
<211> 24
<212> DNA
<213> Vibrio parahaemolyticus

<220>

<400> 57
nattgcattt gaaactggca gact   24

"n" needs explanation (see p.7)

same error in seqs. 170-171, 188, 195

VARIABLE LOCATION SUMMARY DATE: 09/19/2005
PATENT APPLICATION: US/09/937,519 TIME: 10:23:33

Input Set : A:\66741-013; seq. listing
Output Set: N:\CRF4\09192005\I937519.raw

<u>Use of n's or Xaa's(NEW RULES):</u>
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is **MANDATORY** if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:2; N Pos. 5
Seq#:6; N Pos. 24
Seq#:8; N Pos. 29
Seq#:57; N Pos. 1
Seq#:170; N Pos. 18
Seq#:171; N Pos. 19
Seq#:188; N Pos. 24
Seq#:195; N Pos. 24

these sequences lack explanation of "n"

VERIFICATION SUMMARY   DATE: 09/19/2005
PATENT APPLICATION: **US/09/937,519**   TIME: 10:23:33

Input Set : **A:\66741-013; seq. listing**
Output Set: **N:\CRF4\09192005\I937519.raw**

```
L:52 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:2
L:52 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:2
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:730 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:57
L:730 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:57
L:730 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:57
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:1973 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:170
L:1973 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:170
L:1973 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:170
L:1973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:170 after pos.:0
L:1984 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:171
L:1984 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:171
L:1984 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:171
L:1984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:171 after pos.:0
L:2171 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:188
L:2171 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:188
L:2171 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:188
L:2171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188 after pos.:0
L:2248 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:195
L:2248 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:195
L:2248 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:195
L:2248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:195 after pos.:0
```